



RECEIVED  
JUL 26 2001

TECH CENTER 1600/2900

<110> Cahoon, Rebecca E.  
Klein, Theodore M.  
Odell, Joan T.  
Orozco, Emil M. Jr.

<120> PLANT CELL CYCLIN GENES

<130> BB1149 US NA

<150> 60/078,735

<151> 1998 March 20

<150> PCT/US99/06047

<151> 1999 March 19

<160> 32

<170> MICROSOFT OFFICE 97

<210> 1

<211> 1071

<212> DNA

<213> Zea mays

<400> 1

```
ccggaattcc cggggtcgac ccacgcgtcc ggccgcgcgc cgtggcgccc gccgacctcc 60
agctctccgg gtccacgccc tccgacatct acacctacct ccgctccctg gaggtggatc 120
cgcagcggcg gtccagatcc gattacatcg aggcgggtgca ggccggacgtc acggcccaca 180
tgcggagcat cctgcgcgac tggctcgtcg aggtcgccga ggagtacaag ctgcgcgcgg 240
acacgctcta cctcaccatc tcttatgtcg accgcttctt ctccgtcaac gcgctcggcc 300
gtgacaagct gcagctcctt ggcgttgctt ccatgctcat tgccgcgaag ttcgaggaga 360
tcagcccggc gcacccggag gacttctgct acatcacaga caacacctac accaaagagg 420
agctcctcaa gatggagagc gacatactca agcttctcaa gtccgagttg ggcaatccta 480
caatcaagac cttcctgaga cgtttcataa gatctgcccc tgaagacaag aagggtcca 540
tcttgtaaat ggaattcttg gggagctacc tcgctgagct gactctacta gattatggct 600
gctccgggtt cttgcatca gtagttgctg cttcagtcac gtttggtgct aggcctgaca 660
ttgatccaaa taccaatccg tggaacacaa agctgcagaa gatgactggc tacaaagttt 720
ctgaactcaa ggattgcatc gtagccatac atgacttgca gctcaacagg aaatgtccat 780
cattaacggc aattcgagac aagtacaagc agcacaagtt caaatgcgtg tcattgatcc 840
tcgtgcctgt cgtgatccct acttcatact ttgaagactt agctgagtag ctgctctcgg 900
actgtaccgc tgtaaggcta acaatctgag ctctccttga gctcttaggg acaagcagaa 960
aataaccgtt tgatgagctt tcctctcatt taagtagcgt ggtgaaagct atttgtttga 1020
ggttctttag gattaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1071
```

<210> 2

<211> 295

<212> PRT

<213> Zea mays

<400> 2

```
Gly Ile Pro Gly Val Asp Pro Arg Val Arg Pro Arg Ala Val Ala Pro
1           5           10           15

Ala Asp Leu Gln Leu Ser Gly Ser Tyr Ala Ser Asp Ile Tyr Thr Tyr
20           25           30

Leu Arg Ser Leu Glu Val Asp Pro Gln Arg Arg Ser Arg Ser Asp Tyr
35           40           45

Ile Glu Ala Val Gln Ala Asp Val Thr Ala His Met Arg Ser Ile Leu
50           55           60

Val Asp Trp Leu Val Glu Val Ala Glu Glu Tyr Lys Leu Val Ala Asp
65           70           75           80
```

Thr	Leu	Tyr	Leu	Thr	Ile	Ser	Tyr	Val	Asp	Arg	Phe	Leu	Ser	Val	Asn	
				85					90					95		
Ala	Leu	Gly	Arg	Asp	Lys	Leu	Gln	Leu	Leu	Gly	Val	Ala	Ser	Met	Leu	
			100					105					110			
Ile	Ala	Ala	Lys	Phe	Glu	Glu	Ile	Ser	Pro	Pro	His	Pro	Glu	Asp	Phe	
		115					120					125				
Cys	Tyr	Ile	Thr	Asp	Asn	Thr	Tyr	Thr	Lys	Glu	Glu	Leu	Leu	Lys	Met	
	130					135					140					
Glu	Ser	Asp	Ile	Leu	Lys	Leu	Leu	Lys	Phe	Glu	Leu	Gly	Asn	Pro	Thr	
145					150					155					160	
Ile	Lys	Thr	Phe	Leu	Arg	Arg	Phe	Ile	Arg	Ser	Ala	His	Glu	Asp	Lys	
				165					170					175		
Lys	Gly	Ser	Ile	Leu	Leu	Met	Glu	Phe	Leu	Gly	Ser	Tyr	Leu	Ala	Glu	
			180					185					190			
Leu	Ser	Leu	Leu	Asp	Tyr	Gly	Cys	Leu	Arg	Phe	Leu	Pro	Ser	Val	Val	
		195					200					205				
Ala	Ala	Ser	Val	Met	Phe	Val	Ala	Arg	Pro	Asp	Ile	Asp	Pro	Asn	Thr	
	210					215					220					
Asn	Pro	Trp	Asn	Thr	Lys	Leu	Gln	Lys	Met	Thr	Gly	Tyr	Lys	Val	Ser	
225					230					235					240	
Glu	Leu	Lys	Asp	Cys	Ile	Val	Ala	Ile	His	Asp	Leu	Gln	Leu	Asn	Arg	
				245					250					255		
Lys	Cys	Pro	Ser	Leu	Thr	Ala	Ile	Arg	Asp	Lys	Tyr	Lys	Gln	His	Lys	
			260					265					270			
Phe	Lys	Cys	Val	Ser	Leu	Ile	Leu	Val	Pro	Val	Val	Ile	Pro	Thr	Ser	
		275					280					285				
Tyr	Phe	Glu	Asp	Leu	Ala	Glu										
	290					295										

<210> 3  
 <211> 435  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (1)

<220>  
 <221> unsure  
 <222> (86)

<220>  
 <221> unsure  
 <222> (88)

<220>  
 <221> unsure  
 <222> (216)..(217)

<220>  
<221> unsure  
<222> (231)

<220>  
<221> unsure  
<222> (240)

<220>  
<221> unsure  
<222> (307)

<220>  
<221> unsure  
<222> (372)

<220>  
<221> unsure  
<222> (377)

<220>  
<221> unsure  
<222> (427)

---

<400> 3  
nactccatct tcttccatcc atttcctctt tctcgatctg ttccaaattc acttcacaca 60  
caggaaagaa gatggagact cgcgcngncg caaagagaaa ggcaaagcc gccaccatag 120  
tctttgtcga aaaacaatac cccaacaaga ggcagcgggt tgtgttgggt gaacttccca 180  
atttacaaaa ccttattgtc tccgaaactc aaaatnngcg caaagagaag ntcctatgtn 240  
ggaagaatcc caatgagaag aaaccatcac ccacaaacaa caacaccttt ccttcccctc 300  
agatcancga atcttatgat tcggatatcc acgggtatct tcgtgaaatg gagatgcaga 360  
ataagagaag ancaatngtt gatacattga aaaggttaga aaatcggtac ccaaccatgg 420  
agcaatntgg tgatt 435

<210> 4  
<211> 110  
<212> PRT  
<213> Glycine max

<220>  
<221> UNSURE  
<222> (6)

<220>  
<221> UNSURE  
<222> (49)

<220>  
<221> UNSURE  
<222> (54)

<220>  
<221> UNSURE  
<222> (57)

<220>  
<221> UNSURE  
<222> (79)

<220>  
<221> UNSURE  
<222> (101)..(102)

<400> 4  
Met Glu Thr Arg Ala Xaa Ala Lys Arg Lys Ala Asn Ala Ala Thr Ile  
1 5 10 15

Val	Phe	Val	Glu	Lys	Gln	Tyr	Pro	Asn	Lys	Arg	Gln	Arg	Val	Val	Leu
			20					25					30		
Gly	Glu	Leu	Pro	Asn	Leu	Gln	Asn	Leu	Ile	Val	Ser	Glu	Thr	Gln	Asn
		35					40					45			
Xaa	Arg	Lys	Glu	Lys	Xaa	Leu	Cys	Xaa	Lys	Asn	Pro	Asn	Glu	Lys	Lys
		50				55					60				
Pro	Ser	Pro	Thr	Asn	Asn	Asn	Thr	Phe	Pro	Ser	Pro	Gln	Ile	Xaa	Glu
						70				75					80
Ser	Tyr	Asp	Ser	Asp	Ile	His	Gly	Tyr	Leu	Arg	Glu	Met	Glu	Met	Gln
				85					90					95	
Asn	Lys	Arg	Arg	Xaa	Xaa	Val	Asp	Thr	Leu	Lys	Arg	Leu	Glu		
			100					105					110		

<210> 5  
 <211> 847  
 <212> DNA  
 <213> Triticum aestivum

<220>  
 <221> unsure  
 <222> (584)

<220>  
 <221> unsure  
 <222> (686)

<220>  
 <221> unsure  
 <222> (704)

<220>  
 <221> unsure  
 <222> (731)

<220>  
 <221> unsure  
 <222> (748)

<220>  
 <221> unsure  
 <222> (768)

<220>  
 <221> unsure  
 <222> (772)

<220>  
 <221> unsure  
 <222> (781)

<220>  
 <221> unsure  
 <222> (785)

<220>  
 <221> unsure  
 <222> (803)

<220>  
 <221> unsure  
 <222> (806)..(807)

<220>  
 <221> unsure  
 <222> (819)

<220>  
 <221> unsure  
 <222> (825)

<220>  
 <221> unsure  
 <222> (830)

<220>  
 <221> unsure  
 <222> (839)

<400> 5  
 cggaacaggg agagtgggtg tcatgagcca ttctttcagg gaagaaacac aagagataaa 60  
 tctgaaactg ctgactcaaa cactgggtac tatgttggct taaacgttat agacattgac 120  
 aaagataatg gcaatccaca aatgtgtgct tcctatgctg cagagatata cagaaaccta 180  
 atggctgcag agcttataag gagacctaaa tcaaattaca tggagacttt gcaaagggat 240  
 atcacaaagg gcatgcgagg aatcctgatt gattgggctt tgaggttcct ggaggaatat 300  
 aaacttttgc cagacacact atacctcact gtatatctta ttgatcaatt tctttctcgg 360  
 aaatatattg aaagacagaa actacaactt cttggaataa ctagcatgct gattgcctca 420  
 aaatatgaag agatctgtgc gcctcgtgtt gaagaatttt gtttcataac tgataacaca 480  
 tatacaaaaa atcaggtgct gaaaatggag tgtgaagtgc ttaatgatct ggggtttcat 540  
 ctttcagttc ccacaatcaa aacgtttctg aggagattcc ttanagcagc acatgcttct 600  
 caaaaaagcc cttgggcaac tttgggctat ctggggcaat tatcttgccg gagttgacat 660  
 tgaccgatta cagttccctg aaattnaacc tcaatgggtg gaanctcggc gggccctgc 720  
 aaaatggcac ncgacatcag actgcaangg aatccacctc gagcatanac tnaatcaaaa 780  
 nttangtata aagatgcgta cgnatnnatg gaactgacna ggaanacaan ggatccccna 840  
 aggtata 847

<210> 6  
 <211> 211  
 <212> PRT  
 <213> Triticum aestivum

<220>  
 <221> UNSURE  
 <222> (195)

<400> 6  
 Arg Asn Arg Glu Ser Gly Val His Glu Pro Phe Phe Gln Gly Arg Asn  
 1 5 10 15  
 Thr Arg Asp Lys Ser Glu Thr Ala Asp Ser Asn Thr Gly Tyr Tyr Val  
 20 25 30  
 Gly Leu Asn Val Ile Asp Ile Asp Lys Asp Asn Gly Asn Pro Gln Met  
 35 40 45  
 Cys Ala Ser Tyr Ala Ala Glu Ile Tyr Arg Asn Leu Met Ala Ala Glu  
 50 55 60  
 Leu Ile Arg Arg Pro Lys Ser Asn Tyr Met Glu Thr Leu Gln Arg Asp  
 65 70 75 80  
 Ile Thr Lys Gly Met Arg Gly Ile Leu Ile Asp Trp Ala Leu Arg Phe  
 85 90 95

Leu Glu Glu Tyr Lys Leu Leu Pro Asp Thr Leu Tyr Leu Thr Val Tyr  
 100 105 110  
 Leu Ile Asp Gln Phe Leu Ser Arg Lys Tyr Ile Glu Arg Gln Lys Leu  
 115 120 125  
 Gln Leu Leu Gly Ile Thr Ser Met Leu Ile Ala Ser Lys Tyr Glu Glu  
 130 135 140  
 Ile Cys Ala Pro Arg Val Glu Glu Phe Cys Phe Ile Thr Asp Asn Thr  
 145 150 155 160  
 Tyr Thr Lys Asn Gln Val Leu Lys Met Glu Cys Glu Val Leu Asn Asp  
 165 170 175  
 Leu Gly Phe His Leu Ser Val Pro Thr Ile Lys Thr Phe Leu Arg Arg  
 180 185 190  
 Phe Leu Xaa Ala Ala His Ala Ser Gln Lys Ser Pro Trp Ala Thr Leu  
 195 200 205  
 Gly Tyr Leu  
 210

<210> 7  
 <211> 1007  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> unsure  
 <222> (924)

<220>  
 <221> unsure  
 <222> (958)

<220>  
 <221> unsure  
 <222> (971)..(972)

<220>  
 <221> unsure  
 <222> (996)

<400> 7  
 gggagggaat tccttctctc ttttctgttc ggcgcgctgc tcgcgcgcac ccaccgcac 60  
 gccccagtac cccacgctg cacagtgcac gccgacttgc ctccgccttg ctgctgcaag 120  
 tccgcaacca ctggaggaaa aatcttttcc ttacttttcc ttccctttcc cccgcgcat 180  
 gcacgggctc tgattgacgc catgggggac gccgcggcct ccacgtccgc tcccaccacg 240  
 cccacctcca tcctcatctg cctggaagac ggcagcgacc ttctcgccga tgccgacgat 300  
 ggcgcgggca ctgacctcgt tgcgcgccgc gacgaacgtc tgcttgctgt ggaccaggac 360  
 gaggagtatg tagcgctgct cctgtccaag gagagcgctg caggcggcgg cggcccgggtg 420  
 gaggaaatgg aggactggat gaaggccgcg cgctccggat gcgtccgctg gatcatcaag 480  
 accacggcga tgttcgggtt cggcgggaag accgcttacg tggccgtgaa ttacctcgat 540  
 cgcttctctg cgcaacggcg agtcaatagg gagcatgcgt ggggtctgca gctgctcatg 600  
 gtggcgctgca tgcgctggc gaccaagctg gaggagcacc acgctccgcg gctgtcggag 660  
 ttcccgctgg acgcgtgcga gttcgcgttc gacagcgctg ccatacctgcg gatggagctc 720  
 ctgcgtcctg gcacctcga gtggcggatg atcgccgtca ccccttccc ctacatcagc 780  
 tacttcgcgg cgcggttccg ggagacgagc gccgggcgaa tcctcatgcg cgccgtggag 840  
 tgcgtcttcg cggcgatcaa agtgataagc tcggtggagt aacggccgct gaccatcgcc 900  
 gtggcatcca tcctcgtcgc gcgnggccgg gaggagactc ccgccggcag cctggggangc 960  
 gctcaaggcg nntcctcggg tcatcgtgcc cgcaantaga aaacggg 1007

<210> 8  
 <211> 238

<212> PRT  
<213> Zea mays

<220>  
<221> UNSURE  
<222> (227)

<400> 8  
Met Gly Asp Ala Ala Ala Ser Thr Ser Ala Pro Thr Thr Pro Thr Ser  
1 5 10 15  
Ile Leu Ile Cys Leu Glu Asp Gly Ser Asp Leu Leu Ala Asp Ala Asp  
20 25 30  
Asp Gly Ala Gly Thr Asp Leu Val Val Ala Arg Asp Glu Arg Leu Leu  
35 40 45  
Val Val Asp Gln Asp Glu Glu Tyr Val Ala Leu Leu Leu Ser Lys Glu  
50 55 60  
Ser Ala Ser Gly Gly Gly Gly Pro Val Glu Glu Met Glu Asp Trp Met  
65 70 75 80

---

Lys Ala Ala Arg Ser Gly Cys Val Arg Trp Ile Ile Lys Thr Thr Ala  
85 90 95

Met Phe Arg Phe Gly Gly Lys Thr Ala Tyr Val Ala Val Asn Tyr Leu  
100 105 110

Asp Arg Phe Leu Ala Gln Arg Arg Val Asn Arg Glu His Ala Trp Gly  
115 120 125

Leu Gln Leu Leu Met Val Ala Cys Met Ser Leu Ala Thr Lys Leu Glu  
130 135 140

Glu His His Ala Pro Arg Leu Ser Glu Phe Pro Leu Asp Ala Cys Glu  
145 150 155 160

Phe Ala Phe Asp Ser Ala Ser Ile Leu Arg Met Glu Leu Leu Val Leu  
165 170 175

Gly Thr Leu Glu Trp Arg Met Ile Ala Val Thr Pro Phe Pro Tyr Ile  
180 185 190

Ser Tyr Phe Ala Ala Arg Phe Arg Glu Thr Ser Ala Gly Arg Ile Leu  
195 200 205

Met Arg Ala Val Glu Cys Val Phe Ala Ala Ile Lys Val Ile Ser Ser  
210 215 220

Val Glu Xaa Arg Pro Ser Thr Ile Ala Val Ala Ser Ile Leu  
225 230 235

<210> 9  
<211> 510  
<212> DNA  
<213> Oryza sativa

<220>  
<221> unsure  
<222> (424)

<220>  
<221> unsure  
<222> (441)

<400> 9  
 cttacagctt cctcctcgct ttgctggttg cagacgaacg cgggattccg gttcagcttg 60  
 aagacggcgt atgtcgcggt gacgtatctc gatcggttct tggcgcgccg gtgtgtcgat 120  
 agggacaagg agtgggcgct gcagctcctc tcggtggcgt gcctgtcgct ggcggcgaag 180  
 gtggaggagc gccggccgcc gcggtgccg gagttcaagc tggacatgta cgactgcgcg 240  
 tccttgatgc ggatggagct cctcgtcctc accacgctca agtggcagat gatcaccgag 300  
 acacccttct cctacctgaa ctgttcaccg cgaaattccg gcacgacgag cggaaggcat 360  
 cgtcctgcgc gccatcgaat gcattcttcgc tcgatcaaag tcatagctcg gtgggtacag 420  
 catnacgacg gctctagcag natctatcgt cggaacaagg agacggcgct aattagacga 480  
 ctaagtcgctc gtggctctat ggagcactaa 510

<210> 10  
 <211> 181  
 <212> PRT  
 <213> Oryza sativa

<400> 10  
 His Glu Leu Thr Ala Ser Ser Ser Leu Cys Trp Leu Gln Thr Asn Ala  
 1 5 10 15  
 Gly Phe Arg Phe Ser Leu Lys Thr Ala Tyr Val Ala Val Thr Tyr Leu  
 20 25 30

~~Asp Arg Phe Leu Ala Arg Arg Cys Val Asp Arg Asp Lys Glu Trp Ala~~  
~~35 40 45~~

Leu Gln Leu Leu Ser Val Ala Cys Leu Ser Leu Ala Ala Lys Val Glu  
 50 55 60

Glu Arg Arg Pro Pro Arg Leu Pro Glu Phe Lys Leu Asp Met Tyr Asp  
 65 70 75 80

Cys Ala Ser Leu Met Arg Met Glu Leu Leu Val Leu Thr Thr Leu Lys  
 85 90 95

Trp Gln Met Ile Thr Glu Thr Pro Phe Ser Tyr Leu Asn Cys Phe Thr  
 100 105 110

Ala Lys Phe Arg His Asp Glu Arg Lys Ala Ile Val Leu Arg Ala Ile  
 115 120 125

Glu Cys Ile Phe Ala Ser Ile Lys Val Ile Ser Ser Val Gly Tyr Gln  
 130 135 140

Pro Ser Thr Ile Ala Leu Ala Ala Ile Leu Ile Ala Arg Asn Lys Glu  
 145 150 155 160

Thr Ala Pro Asn Leu Asp Glu Leu Ser Val His Arg Leu Ala Pro Trp  
 165 170 175

Gln Leu Met Met Leu  
 180

<210> 11  
 <211> 2259  
 <212> DNA  
 <213> Glycine max

<400> 11  
 acaacttctc ccactcattc atcaacaacc acacacactc tctctcccct ctctgcacca 60  
 aaaccacttc tccggcgaca tctccggtca ggttcgggca acctcatcgg cgaatcggca 120  
 tgccaacaca atgaatgcgg aacctccgct gccgcggcg ctccatcatgt cggtttctctg 180  
 cctctccgac tacgacctcc tctgcggcga ggactcctcc ggaatcctct ccggagagtc 240  
 gcgggagtgc tccttctccg acatcgactc ctcacctcct ccgcccgcgc cgacgacaga 300  
 ggattgttat tcgatcgcca gcttcacga gcacgagcgc aacttcgttc cgggattcga 360  
 gtacctgtcg cggttccaat ctcgctccct ggacgccaac gccagagaag aatcagttgg 420



atggattctc	aaggtacacg	cgtactatgg	ctttcagcct	ttgacggcgt	acctcgccgt	480
caactatatg	gatcggtttt	tggattctcg	ccggttgccg	gaaacaaatg	gggtggcctct	540
gcaacttgta	tctgttgcac	gcttgtcttt	ggcagcaaag	atggaagaac	ctcttggtcc	600
atctctcttg	gaccttcaga	tagaaggtgc	caagtacata	tttgagccga	gaacaattcg	660
taggatggag	ctacttgttc	tccgtgtctt	agattggagg	ctaagatcag	taacaccact	720
ttgcttcctc	gctttctttg	cgtgcaaagt	agattcaact	ggaactttta	tccggttcct	780
tattttccagg	gcaacagaaa	tcacgtatc	taatattcaa	gaggctagct	ttcttgctta	840
ctggccttca	tgcatgtctg	ctgcagccat	actcactgca	gctaatagaa	ttcctaattg	900
gtctgtggtt	aagcccgaaa	atgctgagtc	atgggtgcgag	ggactaagaa	aagaaaaagt	960
aataggggtg	taccagttga	tgcaagagct	tgtgattaac	aataaccaac	ggaaactccc	1020
cttactaaaa	gtgttgccgc	agctgcgagt	aacaactcgg	acccgaatga	gggtcaagtac	1080
tgtatcatca	ttctcatcat	cctcttcaac	ctccttctcc	ttgtcttgta	agaggaggaa	1140
attaaataac	cgtttggtgg	tagatgacaa	aggaaactcc	gagtgaagag	aaaacgaaca	1200
acaataataa	aagaagggaa	gaaaaagaga	gggaataagg	tgggccaagt	tgtctagaaa	1260
cctcaacatt	tttttagagg	tttttgcaat	taaaaaatga	cttgagttag	gggttagatt	1320
ataatagtat	atatatgata	tatctctatc	gtatatacta	agagagtttg	atggggttgg	1380
agtaattttt	atttttatgt	tgggtactta	ttaatatgga	gtttgcagaa	ttcacctagg	1440
gaagagggat	tttgcgacat	gttaccgtgg	gagaggaaat	gagagaagaa	agaagtgaag	1500
cactgaacca	ggggtagaag	aattttaatgt	gatttggtct	tgtaacctgt	gattctgaag	1560
gaaagaattg	agttgcgggc	tggatttcaa	agtttgcatt	aattacttgg	tgaaggagat	1620
gaaagatggt	gggggcaacg	ctgtagagat	tgagaagaag	aaaaagtaga	gagaagggtat	1680
gaaaaactct	ggtgattatt	gaaagttgaa	acttagaagt	ttgaagtgtt	caatgtttat	1740
atcatggtat	tcataagtca	agcaaagctt	catttcttgg	ccagcatcac	tgcttcttca	1800
tcateeaegt	tactactact	ttgatgggac	cctcaacagt	aaagaacaat	tgaagggcaa	1860
taagttgaag	tttggtctaca	aatcgtggac	tttttttgtt	gggtattggc	acgtgtgcag	1920
tccgttctgg	tgcggtgcaa	tgaagtgtgt	acgtgtgatt	tttctttttc	ttgggttttc	1980
tttgcgggag	ctgtttatat	attttttcc	atttttggcc	atgagttttg	gcctaactat	2040
acaggactcc	aatggctggt	gtccgcgcgt	gtgatggaaa	cacgtgtata	tatagggttt	2100
aatttaaaaa	ccttgaattt	ttttatttgt	tttcaagaga	ggagaacctt	ctttcacata	2160
ggggtaaaag	gtctttgggg	ccttttttcc	gtgtgctgtg	tattggattg	attaatatat	2220
aatgacaact	attaatttct	taaaaaaaaa	aaaaaaaaaa			2259

<210> 12  
 <211> 339  
 <212> PRT  
 <213> Glycine max

<400> 12  
 Met Ser Val Ser Cys Leu Ser Asp Tyr Asp Leu Leu Cys Gly Glu Asp  
 1 5 10 15  
 Ser Ser Gly Ile Leu Ser Gly Glu Ser Pro Glu Cys Ser Phe Ser Asp  
 20 25 30  
 Ile Asp Ser Ser Pro Pro Pro Pro Ser Pro Thr Thr Glu Asp Cys Tyr  
 35 40 45  
 Ser Ile Ala Ser Phe Ile Glu His Glu Arg Asn Phe Val Pro Gly Phe  
 50 55 60  
 Glu Tyr Leu Ser Arg Phe Gln Ser Arg Ser Leu Asp Ala Asn Ala Arg  
 65 70 75 80  
 Glu Glu Ser Val Gly Trp Ile Leu Lys Val His Ala Tyr Tyr Gly Phe  
 85 90 95  
 Gln Pro Leu Thr Ala Tyr Leu Ala Val Asn Tyr Met Asp Arg Phe Leu  
 100 105 110  
 Asp Ser Arg Arg Leu Pro Glu Thr Asn Gly Trp Pro Leu Gln Leu Val  
 115 120 125  
 Ser Val Ala Cys Leu Ser Leu Ala Ala Lys Met Glu Glu Pro Leu Val  
 130 135 140

Pro Ser Leu Leu Asp Leu Gln Ile Glu Gly Ala Lys Tyr Ile Phe Glu  
145 150 155 160

Pro Arg Thr Ile Arg Arg Met Glu Leu Leu Val Leu Gly Val Leu Asp  
165 170 175

Trp Arg Leu Arg Ser Val Thr Pro Leu Cys Phe Leu Ala Phe Phe Ala  
180 185 190

Cys Lys Val Asp Ser Thr Gly Thr Phe Ile Arg Phe Leu Ile Ser Arg  
195 200 205

Ala Thr Glu Ile Ile Val Ser Asn Ile Gln Glu Ala Ser Phe Leu Ala  
210 215 220

Tyr Trp Pro Ser Cys Ile Ala Ala Ala Ala Ile Leu Thr Ala Ala Asn  
225 230 235 240

Glu Ile Pro Asn Trp Ser Val Val Lys Pro Glu Asn Ala Glu Ser Trp  
245 250 255

Cys Glu Gly Leu Arg Lys Glu Lys Val Ile Gly Cys Tyr Gln Leu Met  
260 265 270

---

Gln Glu Leu Val Ile Asn Asn Asn Gln Arg Lys Leu Pro Leu Leu Lys  
275 280 285

Val Leu Pro Gln Leu Arg Val Thr Thr Arg Thr Arg Met Arg Ser Ser  
290 295 300

Thr Val Ser Ser Phe Ser Ser Ser Ser Ser Thr Ser Phe Ser Leu Ser  
305 310 315 320

Cys Lys Arg Arg Lys Leu Asn Asn Arg Leu Trp Val Asp Asp Lys Gly  
325 330 335

Asn Ser Glu

<210> 13  
<211> 1994  
<212> DNA  
<213> Glycine max

<400> 13  
gcacgagccg gaatcatgga ttctctgccg gagtgttctt ccgacctcga ttctctgccg 60  
ccgtcggagg cggagtccat cgccggattc atggaagacg agcgcaactt cgtccccgga 120  
ttcgaatacc tcaatagggt ccaatctcgc tctctcgacg cctctgccag agaagaatcc 180  
gttgcatgga ttctcaagggt gcaggcttat tacgcttttc aaccgggtcac ggcttatctt 240  
tccgttaact acttgatag gttcttgaat tctcgaccgt tgccgccgaa aacgaatggg 300  
tggccactgc aacttctctc tgttgcggtg ttgtctttag cagcaaagat ggaggaatct 360  
ctagttccat ctcttttggga ccttcaggta gaaggtgcta aatacgtatt tgaacccaaa 420  
acaattagaa gaatggagct acttggtctg ggcgtgttgg attggaggct aagatcgggt 480  
acccatttta gtttctcga tttctttgcg tgcaagttag attcaactgg gacttttacc 540  
gggttcctca ttacacgtgc tacacaaatt atcttatcta atatacaaga ggctagcttt 600  
cttgcgattt ggccatcatg cattgctgca gcagccattc tccatgcagc aaatgaaatt 660  
cctaattggt ctctcggttag gcctgagcat gcagagtcatt ggtgtgaggg gtttaagaaag 720  
gagaaaatta taggggtgcta ccaattaatg caagaacttg tgattgacaa taaccagagg 780  
aaaccccccta aggtgttacc acagctgcga gtgacaatat ctccggcccat tatgagggtct 840  
agtgtctcat ccttcttagc atcatcctct tcaccttcat catcctcttt gtctttaga 900  
aggaggaaat taaataactc tttgtgggta gacgatgaca aaggaaactc ccaatgaaga 960  
gaaaaagaac aataatagag gaggaaaaaa agaagaataa tgaaataagg tgggtggacgg 1020  
tgggtccagt tgtccagaaa ccgcaaaatt tttaagaggg tttttttgag tataaaatgg 1080  
actagagagt cgagggtgtac attataatat agactatatt ttatgagagt tgcgagcttt 1140  
tattattttg ttggtgggtg ttgccattca tcaatggcat tgcagattcc ctagggaagg 1200  
ggatttttgc aagtgtgtgt ggggtgtgcgt gagagagagg tgggaaatta gatacaaaaga 1260

tgcatttaat ggtttggtcg tgcaagcgtg gaagaaagaa gtgtgtagtt tggaattcaa 1320  
 agatgcgctt gttattgggtg aaagagaaga gaatgggtgt gggacattgc ttcagagctt 1380  
 ggaagaagaa aaaaagcata gtctcagagc agatatcaat aggggtattga aagactttga 1440  
 agtttgagct gtttcttctt attataatgg ggtctctaag tcaagctact catcttggcc 1500  
 agcatgcctc gcttcttcag tttacacgtt acttttggtg gtgtgatggg ataccactag 1560  
 agtacaaaaa aagaaatagc aataaggtga atcttatcac attttgtgga cttatgatga 1620  
 tacgtgtgag acgcctctgg tgtgtgtctc gcacgtgcct acgtgtgatt ttttattttt 1680  
 atttatgttt tagctatggc gggaaatgct ttttatttct ttatttcttt tttggcttga 1740  
 gctttggcct aactatacag gatccattgc ctggtgtcca cgcgtgatgg aaacacgtgt 1800  
 ctatagtttt cattttttgt tttggatttt ttcatttgtt ttcaagagag gagaacctc 1860  
 ttttgttttc tttttagtgc ctaattggct ttgggagaaa ttggagtaaa ggcctttggg 1920  
 gccttttcct gagtgccttg tattgaattc attaataatg acactgttaa ttctataaaa 1980  
 aaaaaaaaaa aaaa 1994

<210> 14  
 <211> 318  
 <212> PRT  
 <213> Glycine max

<400> 14

Ala Arg Ala Gly Ile Met Asp Ser Ser Pro Glu Cys Ser Ser Asp Leu  
 1 5 10 15

Asp Ser Ser Pro Pro Ser Glu Ala Glu Ser Ile Ala Gly Phe Met Glu  
 20 25 30

Asp Glu Arg Asn Phe Val Pro Gly Phe Glu Tyr Leu Asn Arg Phe Gln  
 35 40 45

Ser Arg Ser Leu Asp Ala Ser Ala Arg Glu Glu Ser Val Ala Trp Ile  
 50 55 60

Leu Lys Val Gln Ala Tyr Tyr Ala Phe Gln Pro Val Thr Ala Tyr Leu  
 65 70 75 80

Ser Val Asn Tyr Leu Asp Arg Phe Leu Asn Ser Arg Pro Leu Pro Pro  
 85 90 95

Lys Thr Asn Gly Trp Pro Leu Gln Leu Leu Ser Val Ala Cys Leu Ser  
 100 105 110

Leu Ala Ala Lys Met Glu Glu Ser Leu Val Pro Ser Leu Leu Asp Leu  
 115 120 125

Gln Val Glu Gly Ala Lys Tyr Val Phe Glu Pro Lys Thr Ile Arg Arg  
 130 135 140

Met Glu Leu Leu Val Leu Gly Val Leu Asp Trp Arg Leu Arg Ser Val  
 145 150 155 160

Thr Pro Phe Ser Phe Leu Asp Phe Phe Ala Cys Lys Leu Asp Ser Thr  
 165 170 175

Gly Thr Phe Thr Gly Phe Leu Ile Ser Arg Ala Thr Gln Ile Ile Leu  
 180 185 190

Ser Asn Ile Gln Glu Ala Ser Phe Leu Ala Tyr Trp Pro Ser Cys Ile  
 195 200 205

Ala Ala Ala Ala Ile Leu His Ala Ala Asn Glu Ile Pro Asn Trp Ser  
 210 215 220

Leu Val Arg Pro Glu His Ala Glu Ser Trp Cys Glu Gly Leu Arg Lys  
 225 230 235 240

Glu Lys Ile Ile Gly Cys Tyr Gln Leu Met Gln Glu Leu Val Ile Asp  
 245 250 255  
 Asn Asn Gln Arg Lys Pro Pro Lys Val Leu Pro Gln Leu Arg Val Thr  
 260 265 270  
 Ile Ser Arg Pro Ile Met Arg Ser Ser Val Ser Ser Phe Leu Ala Ser  
 275 280 285  
 Ser Ser Ser Pro Ser Ser Ser Ser Leu Ser Cys Arg Arg Arg Lys Leu  
 290 295 300  
 Asn Asn Ser Leu Trp Val Asp Asp Asp Lys Gly Asn Ser Gln  
 305 310 315

<210> 15  
 <211> 570  
 <212> DNA  
 <213> Triticum aestivum

<220>  
 <221> unsure  
 <222> (499)

<220>  
 <221> unsure  
 <222> (515)..(516)

<220>  
 <221> unsure  
 <222> (558)

<400> 15  
 acagaggttc acctaaaaaa aggctagcag ttcttcccaa agagacaaca gttctaagaa 60  
 aagaagcagg agctgcagct ggtgagcgtc tgtgccctgc tgattgctg caagtacgaa 120  
 gagatttggg ctccagaggt gaacgacttc atattgttct ccgacaacac atatactagg 180  
 gagcagattc tgaggatgga gaaggcaatc ctgaacatgc ttgagtggaa cctgacagtg 240  
 cccacacctt acgtcttctt cgtgtgattc gccaaaggccg catcctcctg agataagaag 300  
 aacggcaagg aggtaaaagg aacaccagat tttaacaaat cctcagatgt agtacgtatc 360  
 tccatttgcc aaacatgatc tattgctgaa ttctgttctc cctgggtgat tgtctaaatg 420  
 gagacacgtc tttttttcgt ggactggcgc tctgtagtat ggacagaata tgtttgattc 480  
 agcacacaag agacaggtna tcaacacaca gtagnnacag tgtctgtaca gccgtataca 540  
 taacattata cttctcanag accactttgg 570

<210> 16  
 <211> 75  
 <212> PRT  
 <213> Triticum aestivum

<220>  
 <221> UNSURE  
 <222> (68)

<400> 16  
 Lys Gln Glu Leu Gln Leu Val Ser Val Cys Ala Leu Leu Ile Ala Cys  
 1 5 10 15  
 Lys Tyr Glu Glu Ile Trp Ala Pro Glu Val Asn Asp Phe Ile Leu Phe  
 20 25 30  
 Ser Asp Asn Thr Tyr Thr Arg Glu Gln Ile Leu Arg Met Glu Lys Ala  
 35 40 45  
 Ile Leu Asn Met Leu Glu Trp Asn Leu Thr Val Pro Thr Pro Tyr Val  
 50 55 60

Phe Leu Val Xaa Phe Ala Lys Ala Ala Ser Ser  
65 70 75

<210> 17  
<211> 1932  
<212> DNA  
<213> Zea mays

<220>  
<221> unsure  
<222> (8)

<220>  
<221> unsure  
<222> (26)

<220>  
<221> unsure  
<222> (159)

<400> 17  
gccacaantg caccgcagac sgcacntsgg cctccctcct ccgtccgtcc gtcctctttcc 60  
ttgtgccttg tctctctcca ctgcgcaactg ccgcattctg cccaagtccc aaacacgcgc 120  
accaagcaaac cagcactcca gccgccagac cagagtctnc ggccgccgcg tcgcacgaca 180  
ggagaggggag agatacgcgg gctttgactt gccgccggtg cgtccgtgcg tgcctgggtgg 240  
gaatagtggg agacgcgggt acagtacagg agccatggcg ccgagctgct acgacgcggc 300  
agcgtccatg ctctctctgcg ccgaggagca cagcagcatc ctgtggtacg aggaggagga 360  
ggagggagctg gaggcggtcg ggagaaggag cggccggtcg ccgggctacg gggacgactt 420  
cggcgccggac ttgttccccg cgcagtcgga ggaatgcgtg gccggtctgg tggagcggga 480  
acgggaccac atgcccggggc cgtgctacgg cgacaggctg cgcggcggcg gcggtgtct 540  
ctgcgtccgc cgggagggcg tcgactggat ttggaaggct tacacgcacc acaggttccg 600  
cctctcactg gcctacttgg cagtgaacta cctcgatcgc ttctctcgcg tgtctgaggt 660  
gccggactgc aaggactgga tgacgcagct cctcgcggtg gcgtgcgttt ctctggccgc 720  
caagatggag gaaaccgccg tcccgcagtg cctggacctt caggaggtcg gagacgcgcg 780  
gtacgtgttc gaggogaaga cgggtccagag gatggagctc ctggttctaa caacctcaa 840  
ctggaggatg catgccgtga cgcggttctc ctacgtggat tacttctcga acaagctcaa 900  
caacggcgcc agcacggcgc cgaggagctg ctggctcttg cagtccgcgg agcttatctt 960  
gcgtgcggcc agaggaaccg gctgcgtcgg gttcaggccg tccgagatcg ccgcgcgggt 1020  
tgcagccgcc gtggccggag acgtggacga cgcggacggc gtcgagaacg cctgctgcgc 1080  
tcacgtagat aaggagcggg tgttgccgtg ccaggaagcg atcgggtcca tggcgtctc 1140  
ggcgccatt gacgacgcta ccgtgccacc gaaatctgcg agacgcagga gctccccctg 1200  
gccgtgcccg cagagccctg tgggggtgct ggacgcggct ccctgcctca gctacaggag 1260  
cgaagaggca gcgactgcga ctgcgactgc gacttctgct gcctcacatg gggcccctgg 1320  
ctcttcaagc tcgtcctcga cctccccggt gaccagcaaa aggaggaaac tcgccagccg 1380  
atgtgatgga tcgtgcagtg accggtcaaa gcgcgcgccc gcccaatgga ccaaagagt 1440  
aattgactag ggcgtctgct tgctttctga tcaaagagt cattgagagg cggcaaaatg 1500  
gaggaataaa ggggattttg gcatgacgag ggcaaaggag ttgatgaata aagacgcgac 1560  
gaggtggaca acacctaaat tgccgatctt ttctttgcaa ggggagtagg ggacctgctt 1620  
gggcctgggg gagggtagta gacagcccag caaaaaacc tggttggtgt gccacgacca 1680  
caatgggcgc gccagccatg gctttgtagg aaacacaagg gcgctagagg agatccgatg 1740  
ggatgactca gaataaagat agtggaggga ccagaccgta tgcagtatgt gcaacaacta 1800  
ggcactggca tgcttatgct caagtaatct gataacttga atgttggtga tccgacaaac 1860  
tgcttctgtg aagagagaaa tgcaggtaga cgatgaatgt atgtgaaaaa aaaaaaaaaa 1920  
aaaaaaaaaa ac 1932

<210> 18  
<211> 388  
<212> PRT  
<213> Zea mays

<400> 18  
Met Ala Pro Ser Cys Tyr Asp Ala Ala Ala Ser Met Leu Leu Cys Ala  
1 5 10 15  
Glu Glu His Ser Ser Ile Leu Trp Tyr Glu Glu Glu Glu Glu Leu  
20 25 30

Glu Ala Val Gly Arg Arg Ser Gly Arg Ser Pro Gly Tyr Gly Asp Asp  
 35 40 45  
 Phe Gly Ala Asp Leu Phe Pro Pro Gln Ser Glu Glu Cys Val Ala Gly  
 50 55 60  
 Leu Val Glu Arg Glu Arg Asp His Met Pro Gly Pro Cys Tyr Gly Asp  
 65 70 75 80  
 Arg Leu Arg Gly Gly Gly Gly Cys Leu Cys Val Arg Arg Glu Ala Val  
 85 90 95  
 Asp Trp Ile Trp Lys Ala Tyr Thr His His Arg Phe Arg Pro Leu Thr  
 100 105 110  
 Ala Tyr Leu Ala Val Asn Tyr Leu Asp Arg Phe Leu Ser Leu Ser Glu  
 115 120 125  
 Val Pro Asp Cys Lys Asp Trp Met Thr Gln Leu Leu Ala Val Ala Cys  
 130 135 140  
 Val Ser Leu Ala Ala Lys Met Glu Glu Thr Ala Val Pro Gln Cys Leu  
 145 150 155 160  
 Asp Leu Gln Glu Val Gly Asp Ala Arg Tyr Val Phe Glu Ala Lys Thr  
 165 170 175  
 Val Gln Arg Met Glu Leu Leu Val Leu Thr Thr Leu Asn Trp Arg Met  
 180 185 190  
 His Ala Val Thr Pro Phe Ser Tyr Val Asp Tyr Phe Leu Asn Lys Leu  
 195 200 205  
 Asn Asn Gly Gly Ser Thr Ala Pro Arg Ser Cys Trp Leu Leu Gln Ser  
 210 215 220  
 Ala Glu Leu Ile Leu Arg Ala Ala Arg Gly Thr Gly Cys Val Gly Phe  
 225 230 235 240  
 Arg Pro Ser Glu Ile Ala Ala Ala Val Ala Ala Ala Val Ala Gly Asp  
 245 250 255  
 Val Asp Asp Ala Asp Gly Val Glu Asn Ala Cys Cys Ala His Val Asp  
 260 265 270  
 Lys Glu Arg Val Leu Arg Cys Gln Glu Ala Ile Gly Ser Met Ala Ser  
 275 280 285  
 Ser Ala Ala Ile Asp Asp Ala Thr Val Pro Pro Lys Ser Ala Arg Arg  
 290 295 300  
 Arg Ser Ser Pro Val Pro Val Pro Gln Ser Pro Val Gly Val Leu Asp  
 305 310 315 320  
 Ala Ala Pro Cys Leu Ser Tyr Arg Ser Glu Glu Ala Ala Thr Ala Thr  
 325 330 335  
 Ala Thr Ala Thr Ser Ala Ala Ser His Gly Ala Pro Gly Ser Ser Ser  
 340 345 350  
 Ser Ser Ser Thr Ser Pro Val Thr Ser Lys Arg Arg Lys Leu Ala Ser  
 355 360 365  
 Arg Cys Asp Gly Ser Cys Ser Asp Arg Ser Lys Arg Ala Pro Ala Gln  
 370 375 380

Trp Thr Lys Glu  
385

<210> 19  
<211> 481  
<212> DNA  
<213> Oryza sativa

<220>  
<221> unsure  
<222> (88)

<220>  
<221> unsure  
<222> (130)

<220>  
<221> unsure  
<222> (251)

<220>  
<221> unsure  
<222> (311)

<220>  
<221> unsure  
<222> (352)

<220>  
<221> unsure  
<222> (359)

<220>  
<221> unsure  
<222> (394)

<220>  
<221> unsure  
<222> (400)

<220>  
<221> unsure  
<222> (408)

<220>  
<221> unsure  
<222> (410)

<220>  
<221> unsure  
<222> (415)

<220>  
<221> unsure  
<222> (420)

<220>  
<221> unsure  
<222> (426)

<220>  
<221> unsure  
<222> (432) .. (433)

<220>  
<221> unsure  
<222> (448)

<220>  
<221> unsure  
<222> (457)

<220>  
<221> unsure  
<222> (461)..(462)

<220>  
<221> unsure  
<222> (470)

<220>  
<221> unsure  
<222> (475)

<400> 19  
cttacatgta agctcgtgcc gaattcggca cgagcttaca cgagcgcaac ccatggggcgc 60  
cgcggtgct cgccatcagc tgcctcance tcgcccgaac gatgcagcgc gccgcccga 120  
~~teteeggegn cgacatccag agggggcgagg agttcatgtt cgacgaggcg aaaatccagc 180~~  
gcatggagca gatggtgctc aacgcgctgg agtggcggac gcgctccgtc acgcccgtcg 240  
ccttcctcgg nttctttctc tccgcgtggt tcccgcaagc cgcggcaccc ggcgctgctc 300  
gatgccatca nggcccgcgc gtcgagctcc tcctccgcgt ctaagccggg angtgaacna 360  
tggtgggagt tctccccctt cggtgggcgg ccgncgcggn tctcctcnen gccgncggan 420  
aaggcntccg gnngcccacaa ctccttcnct tccaaanctg nnggccccgn ttgncccct 480  
t 481

<210> 20  
<211> 110  
<212> PRT  
<213> Oryza sativa

<220>  
<221> UNSURE  
<222> (26)

<220>  
<221> UNSURE  
<222> (40)

<220>  
<221> UNSURE  
<222> (100)

<400> 20  
Ala Arg Ala Glu Phe Gly Thr Ser Leu His Glu Arg Asn Pro Trp Ala  
1 5 10 15  
Pro Arg Leu Leu Ala Ile Ser Cys Leu Xaa Leu Ala Ala Lys Met Gln  
20 25 30  
Arg Ala Ala Ala Ile Ser Ala Xaa Asp Ile Gln Arg Gly Glu Glu Phe  
35 40 45  
Met Phe Asp Glu Ala Lys Ile Gln Arg Met Glu Gln Met Val Leu Asn  
50 55 60  
Ala Leu Glu Trp Arg Thr Arg Ser Val Thr Pro Leu Ala Phe Leu Gly  
65 70 75 80  
Phe Phe Leu Ser Ala Trp Phe Pro Gln Ala Ala Ala Pro Gly Ala Ala  
85 90 95



Arg Cys His Xaa Gly Arg Ala Val Glu Leu Leu Leu Arg Val  
100 105 110

<210> 21  
<211> 789  
<212> DNA  
<213> Triticum aestivum

<400> 21  
cacctgaggg cgactcgagg gtgccctcgc cccgtccgcc gtgaccaccc ctcttcggat 60  
ctcaccgcct cgacccaaat gtgatttgag gcaaattctg cgtttgaggc aaggacaata 120  
aaagtgatgg agctttttggt cttcagcacc ttgaaatgga ggatgcaagc tgttactgct 180  
tgctcgttta ttgactactt cctttgcaaa ttcaatgac atgacacacc ctccatgctt 240  
gcattctcct gctcaactga cctcatcctg agcacaacta agtgagctga ttttttggtg 300  
ttcagacatt cagagattgc tgggaagtgtt gcacttcctt catttgggga gcacaagact 360  
tcagttgtcg aaatggctac aactaattgc aagtatataa acaaggaggat gtgatgtgac 420  
aggaaagatc ctgatgaagt gcttccttta tggaaatgcct atctgaagtt tggactaaga 480  
gacatgcttt aattggctta gtaaaaaata cttgctaaag agaaataaga ttcaaagtag 540  
atgtttttat tgtagattag gatattgtgtg ttctgccacc ggttcgactt ctcatattag 600  
aaggcaagca gttagttcat atcttactac tttgcactat tgtagatgga tggtagaggga 660  
ttgagaggct actactatta atgtgcgtaa actttgcac tttagctctc taaatgaaac 720  
cggatgatgt taacctgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780  
aaaaaaaaa

<210> 22  
<211> 163  
<212> PRT  
<213> Triticum aestivum

<220>  
<221> UNSURE  
<222> (28)

<220>  
<221> UNSURE  
<222> (95)

<220>  
<221> UNSURE  
<222> (138)

<400> 22  
His Leu Arg Ala Thr Arg Gly Cys Pro Arg Pro Val Arg Arg Asp His  
1 5 10 15  
Pro Ser Ser Asp Leu Thr Ala Ser Thr Lys Met Xaa Phe Glu Ala Asn  
20 25 30  
Ser Ala Phe Glu Ala Arg Thr Ile Lys Val Met Glu Leu Leu Val Phe  
35 40 45  
Ser Thr Leu Lys Trp Arg Met Gln Ala Val Thr Ala Cys Ser Phe Ile  
50 55 60  
Asp Tyr Phe Leu Cys Lys Phe Asn Asp His Asp Thr Pro Ser Met Leu  
65 70 75 80  
Ala Phe Ser Cys Ser Thr Asp Leu Ile Leu Ser Thr Thr Lys Xaa Ala  
85 90 95  
Asp Phe Leu Val Phe Arg His Ser Glu Ile Ala Gly Ser Val Ala Leu  
100 105 110  
Pro Ser Phe Gly Glu His Lys Thr Ser Val Val Glu Met Ala Thr Thr  
115 120 125

Asn Cys Lys Tyr Ile Asn Lys Gly Val Xaa Cys Asp Arg Lys Asp Pro  
 130 135 140

Asp Glu Val Leu Pro Leu Trp Asn Ala Tyr Leu Lys Phe Gly Leu Arg  
 145 150 155 160

Asp Met Leu

<210> 23  
 <211> 603  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> unsure  
 <222> (441)

<220>  
 <221> unsure  
 <222> (447)

<220>  
 <221> unsure  
 <222> (485)

<220>  
 <221> unsure  
 <222> (498)

<220>  
 <221> unsure  
 <222> (528)

<220>  
 <221> unsure  
 <222> (553)

<220>  
 <221> unsure  
 <222> (560)

<220>  
 <221> unsure  
 <222> (576) .. (577)

<220>  
 <221> unsure  
 <222> (598)

<400> 23  
 aacagaattc ggcacgagcc gcggtcggct gggtttcacg cgccgcggcg cggctaggct 60  
 tctccgcgct caccgcgcgc ctccgcgcgc cctacctcga ccgctgcttc ctccccgggg 120  
 gcgcgctccg gctcggcgac cagccctgga tggcgcgcct agccgcgcgc acctgcttcg 180  
 cgctcgccgc caaggtcgag gagacgcgcg tgccgcgcct cctcgacctc cagctctacg 240  
 ccgccgctga cgccgcggat ccgtacgtat tcgaggccaa gacggtgcgc cggatggagc 300  
 tgctcgctgct ctccgcgctt ggggtggcgga tgcaccctgt cacgcccttc tcctacctcc 360  
 agcccgctct cgccgacgct gcgacgcgcc tgcgtagctg cgagggcgct ctgctcgcgc 420  
 tcatggccga ctggaggtgg cctcggcacc ggccttcggc gtgggcccgc gccgcgttgc 480  
 tgatcacagc cgccgcgggc gacggcggcg acggcgacgg cgacacggag ctctgggcgc 540  
 tcatcaatgc ccccgaggac aagaccgcgc agtgtgccaa gatcatctcc gaggtgacgg 600  
 gcatgagctt cctcgccctgc gatgtcggcg tgagcgccgg aaataagcgt aagcacgcgc 660  
 cggcgcagtt gtactcgccg ccgccgagcc cgagcgccgt gatcggcgcg ctgtcctgct 720  
 tcagctgcga gagctcgacg tccgccaccg ctatggctgc ggcggtcggc ccgtgggcgc 780  
 cgtcggcgct cgtgtccgtg tcgtcctctc cagagccacc aggtcgggccc cccaagcgcg 840

cagcggcggc gtcggcgtcg gcgtcggcgt cagccggggg cgcgccaccg gtccagggtcc 900  
 cgcacacagct acccccccgc gaggagagcc gcgacgcctg gccgtccacc tgcgccgcgt 960  
 gacgcaccgt gccggaaacg gtgcctatgg cgagaccgcc gttcgggtggc ggtggagaat 1020  
 ggagaacaag gagcatcatt ggctcgcgtc ggtgagcagg agaacgaact attttgccca 1080  
 ttgccgtgac agatgggggg tggtcactgc gtggagccgc gctgancaat ga 1132

<210> 24  
 <211> 318  
 <212> PRT  
 <213> Zea mays

<400> 24

Asn Ser Ala Arg Ala Ala Val Gly Trp Val Ser Arg Ala Ala Ala Arg  
 1 5 10 15

Leu Gly Phe Ser Ala Leu Thr Ala Ala Leu Ala Ala Tyr Leu Asp  
 20 25 30

Arg Cys Phe Leu Pro Gly Gly Ala Leu Arg Leu Gly Asp Gln Pro Trp  
 35 40 45

Met Ala Arg Leu Ala Ala Val Thr Cys Phe Ala Leu Ala Ala Lys Val  
 50 55 60

Glu Glu Thr Arg Val Pro Pro Leu Leu Asp Leu Gln Leu Tyr Ala Ala  
 65 70 75 80

Ala Asp Ala Ala Asp Pro Tyr Val Phe Glu Ala Lys Thr Val Arg Arg  
 85 90 95

Met Glu Leu Leu Val Leu Ser Ala Leu Gly Trp Arg Met His Pro Val  
 100 105 110

Thr Pro Phe Ser Tyr Leu Gln Pro Val Leu Ala Asp Ala Ala Thr Arg  
 115 120 125

Leu Arg Ser Cys Glu Gly Val Leu Leu Ala Val Met Ala Asp Trp Arg  
 130 135 140

Trp Pro Arg His Arg Pro Ser Ala Trp Ala Ala Ala Ala Leu Leu Ile  
 145 150 155 160

Thr Ala Ala Ala Gly Asp Gly Gly Asp Gly Asp Gly Asp Thr Glu Leu  
 165 170 175

Leu Ala Leu Ile Asn Ala Pro Glu Asp Lys Thr Ala Glu Cys Ala Lys  
 180 185 190

Ile Ile Ser Glu Val Thr Gly Met Ser Phe Leu Ala Cys Asp Val Gly  
 195 200 205

Val Ser Ala Gly Asn Lys Arg Lys His Ala Ala Ala Gln Leu Tyr Ser  
 210 215 220

Pro Pro Pro Ser Pro Ser Gly Val Ile Gly Ala Leu Ser Cys Phe Ser  
 225 230 235 240

Cys Glu Ser Ser Thr Ser Ala Thr Ala Met Ala Ala Ala Val Gly Pro  
 245 250 255

Trp Ala Pro Ser Ala Ser Val Ser Val Ser Ser Ser Pro Glu Pro Pro  
 260 265 270

Gly Arg Ala Pro Lys Arg Ala Ala Ala Ala Ser Ala Ser Ala Ser Ala  
 275 280 285

Ser Ala Gly Val Ala Pro Pro Val Gln Val Pro His Gln Leu Pro Pro  
290 295 300

Asp Glu Glu Ser Arg Asp Ala Trp Pro Ser Thr Cys Ala Ala  
305 310 315

<210> 25  
<211> 674  
<212> DNA  
<213> Glycine max

<220>  
<221> unsure  
<222> (527)

<220>  
<221> unsure  
<222> (561)

<220>  
<221> unsure  
<222> (640)

---

<220>  
<221> unsure  
<222> (643)

<400> 25  
cactcactca ccccttcctt tctaaactcct caaattgtgt gttctgagaa tggaaatgcc 60  
tccttctcca tcggggcatt ccgcactctc catcccataa aagtcccaga tccaagatgg 120  
cttaccacca tcaaaaatcc cttttggaca ccctatactg ctccgaagag cattggatag 180  
gggaaggtga atttgaccaa gcagaggagg agtacggtaa cagtaatagc aatagtagca 240  
gcaccttagt aaacaactcc cctgagtcct cccctcattt gttgctcgaa agcgacatgt 300  
tttgggacga acaagagttg gcacgcgtgt tggagaaaga acaacacaac ccactaagca 360  
cttgctgtct ccaaagcaac cctgccttgg aggggtgctcg catagaagcc gtggagtggg 420  
ttctcaaagt aaacgcccac tactccttct ctgccctcac cgctgttctt gctgtcaact 480  
actttgaccg ttttctcttc agcttccgct ttcagaatga cattaancca tggatgactc 540  
ggggtcgctg ccgtcgcttg nctctccctc gctgccaaag tgggcgagac acacgttccc 600  
tttcttattt gacccttcaa caaagtggga ggaggagtan atnctttgtt ccaagccaaa 660  
gacgattaaa aaag 674

<210> 26  
<211> 186  
<212> PRT  
<213> Glycine max

<220>  
<221> UNSURE  
<222> (137)

<220>  
<221> UNSURE  
<222> (149)

<220>  
<221> UNSURE  
<222> (175)..(176)

<400> 26  
Met Ala Tyr His His Gln Lys Ser Leu Leu Asp Thr Leu Tyr Cys Ser  
1 5 10 15  
Glu Glu His Trp Ile Gly Glu Gly Glu Phe Asp Gln Ala Glu Glu Glu  
20 25 30

Tyr Gly Asn Ser Asn Ser Asn Ser Ser Ser Thr Leu Val Asn Asn Ser  
 35 40 45  
 Pro Glu Ser Ser Pro His Leu Leu Leu Glu Ser Asp Met Phe Trp Asp  
 50 55 60  
 Glu Gln Glu Leu Ala Ser Leu Leu Glu Lys Glu Gln His Asn Pro Leu  
 65 70 75 80  
 Ser Thr Cys Cys Leu Gln Ser Asn Pro Ala Leu Glu Gly Ala Arg Ile  
 85 90 95  
 Glu Ala Val Glu Trp Ile Leu Lys Val Asn Ala His Tyr Ser Phe Ser  
 100 105 110  
 Ala Leu Thr Ala Val Leu Ala Val Asn Tyr Phe Asp Arg Phe Leu Phe  
 115 120 125  
 Ser Phe Arg Phe Gln Asn Asp Ile Xaa Pro Trp Met Thr Arg Gly Arg  
 130 135 140  
 Cys Arg Arg Leu Xaa Leu Pro Arg Cys Gln Ser Gly Arg Asp Thr Arg  
 145 150 155 160  
 Ser Leu Ser Tyr Leu Thr Leu Gln Gln Ser Gly Arg Arg Ser Xaa Xaa  
 165 170 175  
 Phe Val Pro Ser Gln Arg Arg Leu Lys Lys  
 180 185

<210> 27  
 <211> 554  
 <212> DNA  
 <213> Glycine max

<400> 27  
 ctccctttca cttttcttca tagcctacca cttttctgct ttcattctact ctcactttctc 60  
 ttcacacact gagacacaca gagagagaaa aataaagggt gtgatgggtg tcttactgag 120  
 tgttttcttt ttataatgaa caaagaactg cacaccctct tcttcacoga agaagaagat 180  
 ggcaattcag caccacaatg accaactaga gcataatgaa aatgtctcat ctgtccttga 240  
 tgccctttac tgtgacgaag gaaagtggga agaggaagag gaggagaaaag aagaagaaga 300  
 agatgaagggt gaaaatgaaa gtgaagtgc aacaaacact gcaacttgtc ttttccctct 360  
 gctcttggtg gagcaagact tgttctggga agatgaggaa ctaactcta tcttttccaa 420  
 agagaagggt caacatgaag aagcctatgg tataacaatc tgaacagtga tgtgtataac 480  
 aacaacaaca atactagtat ataatgtgat ttggctcttg ctcttcagct cgtcggagcg 540  
 tgatgatgct gaat 554

<210> 28  
 <211> 94  
 <212> PRT  
 <213> Glycine max

<400> 28  
 Met Ala Ile Gln His His Asn Asp Gln Leu Glu His Asn Glu Asn Val  
 1 5 10 15  
 Ser Ser Val Leu Asp Ala Leu Tyr Cys Asp Glu Gly Lys Trp Glu Glu  
 20 25 30  
 Glu Glu Glu Glu Lys Glu Glu Glu Glu Asp Glu Gly Glu Asn Glu Ser  
 35 40 45  
 Glu Val Thr Thr Asn Thr Ala Thr Cys Leu Phe Pro Leu Leu Leu Leu  
 50 55 60

Glu Gln Asp Leu Phe Trp Glu Asp Glu Glu Leu Asn Ser Ile Phe Ser  
65 70 75 80

Lys Glu Lys Val Gln His Glu Glu Ala Tyr Gly Ile Thr Ile  
85 90

<210> 29  
<211> 372  
<212> PRT  
<213> Catharanthus roseus

<400> 29

Met Ala Asp Lys Glu Asn Cys Ile Arg Val Thr Arg Leu Ala Lys Lys  
1 5 10 15

Arg Ala Val Glu Ala Met Ala Ala Ser Glu Gln Gln Arg Pro Ser Lys  
20 25 30

Lys Arg Val Val Leu Gly Glu Leu Lys Asn Leu Ser Ser Asn Ile Ser  
35 40 45

Ser Ile Gln Thr Tyr Asp Phe Ser Ser Gly Pro Gln Lys Gln Gln Lys  
50 55 60

Asn Lys Asn Lys Arg Lys Ala Lys Glu Ser Leu Gly Phe Glu Val Lys  
65 70 75 80

Glu Lys Lys Val Glu Glu Ala Gly Ile Asp Val Phe Ser Gln Ser Asp  
85 90 95

Asp Pro Gln Met Cys Gly Ala Tyr Val Ser Asp Ile Tyr Glu Tyr Leu  
100 105 110

His Lys Met Glu Met Glu Thr Lys Arg Arg Pro Leu Pro Asp Tyr Leu  
115 120 125

Asp Lys Val Gln Lys Asp Val Thr Ala Asn Met Arg Gly Val Leu Ile  
130 135 140

Asp Trp Leu Val Glu Val Ala Glu Glu Tyr Lys Leu Leu Pro Asp Thr  
145 150 155 160

Leu Tyr Leu Thr Val Ser Tyr Ile Asp Arg Phe Leu Ser Met Asn Ala  
165 170 175

Leu Ser Arg Gln Lys Leu Gln Leu Leu Gly Val Ser Ser Met Leu Ile  
180 185 190

Ala Ser Lys Tyr Glu Glu Ile Ser Pro Pro His Val Glu Asp Phe Cys  
195 200 205

Tyr Ile Thr Asp Asn Thr Tyr Lys Lys Glu Glu Val Val Lys Met Glu  
210 215 220

Ala Asp Val Leu Lys Phe Leu Lys Phe Glu Met Gly Asn Pro Thr Ile  
225 230 235 240

Lys Thr Phe Leu Arg Arg Leu Thr Arg Val Val Gln Asp Gly Asp Lys  
245 250 255

Asn Pro Asn Leu Gln Phe Glu Phe Leu Gly Tyr Tyr Leu Ala Glu Leu  
260 265 270

Ser Leu Leu Asp Tyr Gly Cys Val Lys Phe Leu Pro Ser Leu Ile Ala  
275 280 285

Ser Ser Val Ile Phe Leu Ser Arg Phe Thr Leu Gln Pro Lys Val His  
 290 295 300  
 Pro Trp Asn Ser Leu Leu Gln His Asn Ser Gly Tyr Lys Pro Ala Asp  
 305 310 315 320  
 Leu Lys Glu Cys Val Leu Ile Ile His Asp Leu Gln Leu Ser Lys Arg  
 325 330 335  
 Gly Ser Ser Leu Val Ala Val Arg Asp Lys Tyr Lys Gln His Lys Phe  
 340 345 350  
 Lys Cys Val Ser Thr Leu Thr Ala Pro Pro Ser Ile Pro Asp Glu Phe  
 355 360 365  
 Phe Glu Asp Ile  
 370  
 <210> 30  
 <211> 335  
 <212> PRT  
 <213> Arabidopsis thaliana

---

<400> 30  
 Met Arg Ser Tyr Arg Phe Ser Asp Tyr Leu His Met Ser Val Ser Phe  
 1 5 10 15  
 Ser Asn Asp Met Asp Leu Phe Cys Gly Glu Asp Ser Gly Val Phe Ser  
 20 25 30  
 Gly Glu Ser Thr Val Asp Phe Ser Ser Ser Glu Val Asp Ser Trp Pro  
 35 40 45  
 Gly Asp Ser Ile Ala Cys Phe Ile Glu Asp Glu Arg His Phe Val Pro  
 50 55 60  
 Gly His Asp Tyr Leu Ser Arg Phe Gln Thr Arg Ser Leu Asp Ala Ser  
 65 70 75 80  
 Ala Arg Glu Asp Ser Val Ala Trp Ile Leu Lys Val Gln Ala Tyr Tyr  
 85 90 95  
 Asn Phe Gln Pro Leu Thr Ala Tyr Leu Ala Val Asn Tyr Met Asp Arg  
 100 105 110  
 Phe Leu Tyr Ala Arg Arg Leu Pro Glu Thr Ser Gly Trp Pro Met Gln  
 115 120 125  
 Leu Leu Ala Val Ala Cys Leu Ser Leu Ala Ala Lys Met Glu Glu Ile  
 130 135 140  
 Leu Val Pro Ser Leu Phe Asp Phe Gln Val Ala Gly Val Lys Tyr Leu  
 145 150 155 160  
 Phe Glu Ala Lys Thr Ile Lys Arg Met Glu Leu Leu Val Leu Ser Val  
 165 170 175  
 Leu Asp Trp Arg Leu Arg Ser Val Thr Pro Phe Asp Phe Ile Ser Phe  
 180 185 190  
 Phe Ala Tyr Lys Ile Asp Pro Ser Gly Thr Phe Leu Gly Phe Phe Ile  
 195 200 205  
 Ser His Ala Thr Glu Ile Ile Leu Ser Asn Ile Lys Glu Ala Ser Phe  
 210 215 220

Leu Glu Tyr Trp Pro Ser Ser Ile Ala Ala Ala Ala Ile Leu Cys Val  
 225 230 235 240  
 Ala Asn Glu Leu Pro Ser Leu Ser Ser Val Val Asn Pro His Glu Ser  
 245 250 255  
 Pro Glu Thr Trp Cys Asp Gly Leu Ser Lys Glu Lys Ile Val Arg Cys  
 260 265 270  
 Tyr Arg Leu Met Lys Ala Met Ala Ile Glu Asn Asn Arg Leu Asn Thr  
 275 280 285  
 Pro Lys Val Ile Ala Lys Leu Arg Val Ser Val Arg Ala Ser Ser Thr  
 290 295 300  
 Leu Thr Arg Pro Ser Asp Glu Ser Ser Ser Pro Cys Lys Arg Arg Lys  
 305 310 315 320  
 Leu Ser Gly Tyr Ser Trp Val Gly Asp Glu Thr Ser Thr Ser Asn  
 325 330 335

<210> 31

<211> 354

<212> PRT

<213> Nicotiana tabacum

<400> 31

Met Ala Ala Asp Asn Ile Tyr Asp Phe Val Ala Ser Asn Leu Leu Cys  
 1 5 10 15  
 Thr Glu Thr Lys Ser Leu Cys Phe Asp Asp Val Asp Ser Leu Thr Ile  
 20 25 30  
 Ser Gln Gln Asn Ile Glu Thr Lys Ser Lys Asp Leu Ser Phe Asn Asn  
 35 40 45  
 Gly Ile Arg Ser Glu Pro Leu Ile Asp Leu Pro Ser Leu Ser Glu Glu  
 50 55 60  
 Cys Leu Ser Phe Met Val Gln Arg Glu Met Glu Phe Leu Pro Lys Asp  
 65 70 75 80  
 Asp Tyr Val Glu Arg Leu Arg Ser Gly Asp Leu Asp Leu Ser Val Arg  
 85 90 95  
 Lys Glu Ala Leu Asp Trp Ile Leu Lys Ala His Met His Tyr Gly Phe  
 100 105 110  
 Gly Glu Leu Ser Phe Cys Leu Ser Ile Asn Tyr Leu Asp Arg Phe Leu  
 115 120 125  
 Ser Leu Tyr Glu Leu Pro Arg Ser Lys Thr Trp Thr Val Gln Leu Leu  
 130 135 140  
 Ala Val Ala Cys Leu Ser Leu Ala Ala Lys Met Glu Glu Ile Asn Val  
 145 150 155 160  
 Pro Leu Thr Val Asp Leu Gln Val Gly Asp Pro Lys Phe Val Phe Glu  
 165 170 175  
 Gly Lys Thr Ile Gln Arg Met Glu Leu Leu Val Leu Ser Thr Leu Lys  
 180 185 190  
 Trp Arg Met Gln Ala Tyr Thr Pro Tyr Thr Phe Ile Asp Tyr Phe Met  
 195 200 205



Arg Lys Met Asn Gly Asp Gln Ile Pro Ser Arg Pro Leu Ile Ser Gly  
 210 215 220  
 Ser Met Gln Leu Ile Leu Ser Ile Ile Arg Ser Ile Asp Phe Leu Glu  
 225 230 235 240  
 Phe Arg Ser Ser Glu Ile Ala Ala Ser Val Ala Met Ser Val Ser Gly  
 245 250 255  
 Glu Ile Gln Ala Lys Asp Ile Asp Lys Ala Met Pro Cys Phe Phe Ile  
 260 265 270  
 His Leu Asp Lys Gly Arg Val Gln Lys Cys Val Glu Leu Ile Gln Asp  
 275 280 285  
 Leu Thr Thr Ala Thr Ile Thr Thr Ala Ala Ala Ser Leu Val Pro  
 290 295 300  
 Gln Ser Pro Ile Gly Val Leu Glu Ala Ala Ala Cys Leu Ser Tyr Lys  
 305 310 315 320  
 Ser Gly Asp Glu Arg Thr Val Gly Ser Cys Thr Thr Ser Ser His Thr  
 325 330 335  
 Lys Arg Arg Lys Leu Asp Thr Ser Ser Leu Glu His Gly Thr Ser Glu  
 340 345 350

Lys Leu

<210> 32  
 <211> 373  
 <212> PRT  
 <213> Nicotiana tabacum

<400> 32  
 Met Ala Ile Glu His Asn Glu Gln Gln Glu Leu Ser Gln Ser Phe Leu  
 1 5 10 15  
 Leu Asp Ala Leu Tyr Cys Glu Glu Glu Glu Glu Lys Trp Gly Asp Leu  
 20 25 30  
 Val Asp Asp Glu Thr Ile Ile Thr Pro Leu Ser Ser Glu Val Thr Thr  
 35 40 45  
 Thr Thr Thr Thr Thr Thr Lys Pro Asn Ser Leu Leu Pro Leu Leu Leu  
 50 55 60  
 Leu Glu Gln Asp Leu Phe Trp Glu Asp Glu Glu Leu Leu Ser Leu Phe  
 65 70 75 80  
 Ser Lys Glu Lys Glu Thr His Cys Trp Phe Asn Ser Phe Gln Asp Asp  
 85 90 95  
 Ser Leu Leu Cys Ser Ala Arg Val Asp Ser Val Glu Trp Ile Leu Lys  
 100 105 110  
 Val Asn Gly Tyr Tyr Gly Phe Ser Ala Leu Thr Ala Val Leu Ala Ile  
 115 120 125  
 Asn Tyr Phe Asp Arg Phe Leu Thr Ser Leu His Tyr Gln Lys Asp Lys  
 130 135 140  
 Pro Trp Met Ile Gln Leu Ala Ala Val Thr Cys Leu Ser Leu Ala Ala  
 145 150 155 160

Lys Val Glu Glu Thr Gln Val Pro Leu Leu Leu Asp Phe Gln Val Glu  
 165 170 175  
 Asp Ala Lys Tyr Val Phe Glu Ala Lys Thr Ile Gln Arg Met Glu Leu  
 180 185 190  
 Leu Val Leu Ser Ser Leu Lys Trp Arg Met Asn Pro Val Thr Pro Leu  
 195 200 205  
 Ser Phe Leu Asp His Ile Ile Arg Arg Leu Gly Leu Arg Asn Asn Ile  
 210 215 220  
 His Trp Glu Phe Leu Arg Arg Cys Glu Asn Leu Leu Leu Ser Ile Met  
 225 230 235 240  
 Ala Asp Cys Arg Phe Val Arg Tyr Met Pro Ser Val Leu Ala Thr Ala  
 245 250 255  
 Ile Met Leu His Val Ile His Gln Val Glu Pro Cys Asn Ser Val Asp  
 260 265 270  
 Tyr Gln Asn Gln Leu Leu Gly Val Leu Lys Ile Asn Lys Glu Lys Val  
 275 280 285  
 Asn Asn Cys Phe Glu Leu Ile Ser Glu Val Cys Ser Lys Pro Ile Ser  
 290 295 300  
 His Lys Arg Lys Tyr Glu Asn Pro Ser His Ser Pro Ser Gly Val Ile  
 305 310 315 320  
 Asp Pro Ile Tyr Ser Ser Glu Ser Ser Asn Asp Ser Trp Asp Leu Glu  
 325 330 335  
 Ser Thr Ser Ser Tyr Phe Pro Val Phe Lys Lys Ser Arg Val Gln Glu  
 340 345 350  
 Gln Gln Met Lys Leu Ala Ser Ser Ile Ser Arg Val Phe Val Glu Ala  
 355 360 365  
 Val Gly Ser Pro His  
 370